

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Glimcher, Laurie H. et al.

(ii) TITLE OF INVENTION: Human c-Maf Compositions and
Methods of Use Thereof

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(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: LAHIVE & COCKFIELD, LLP

(B) STREET: 28 State Street

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: USA

(F) ZIP: 02109

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

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(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

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(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/030,579

(B) FILING DATE: 2-FEB-1998

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kara, Catherine J.

(B) REGISTRATION NUMBER: 41,106

(C) REFERENCE/DOCKET NUMBER: HUI-027CP

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400

(B) TELEFAX: (617) 742-4214

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1203 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1;

	ATG	GCA	TCA	GAA	CTG	GCA	ATG	AGC	AAC	TCC	GAC	CTG	CCC	ACC	AGT	CCC	48
10	Met	Ala	Ser	Glu	Leu	Ala	Met	Ser	Asn	Ser	Asp	Leu	Pro	Thr	Ser	Pro	
	1				5					10					15		
	CTG	GCC	ATG	GAA	TAT	GTT	AAT	GAC	TTC	GAT	CTG	ATG	AAG	TTT	GAA	GTG	96
15	Leu	Ala	Met	Glu	Tyr	Val	Asn	Asp	Phe	Asp	Leu	Met	Lys	Phe	Glu	Val	
				20					25					30			
	AAA	AAG	GAA	CCG	GTG	GAG	ACC	GAC	CGC	ATC	ATC	AGC	CAG	TGC	GGC	CGT	144
20	Lys	Lys	Glu	Pro	Val	Glu	Thr	Asp	Arg	Ile	Ile	Ser	Gln	Cys	Gly	Arg	
			35					40					45				
	CTC	ATC	GCC	GGG	GGC	TCG	CTG	TCC	TCC	ACC	CCC	ATG	AGC	ACG	CCC	TGC	192
25	Leu	Ile	Ala	Gly	Gly	Ser	Leu	Ser	Ser	Thr	Pro	Met	Ser	Thr	Pro	Cys	
		50					55					60					
	AGC	TCG	GTG	CCC	CCG	TCC	CCC	AGC	TTC	TCG	GCG	CCC	AGC	CCG	GGC	TCG	240
30	Ser	Ser	Val	Pro	Pro	Ser	Pro	Ser	Phe	Ser	Ala	Pro	Ser	Pro	Gly	Ser	
	65					70					75					80	
	CGA	GGC	GAA	CAG	AAG	GCG	CAC	CTG	GAA	GAC	TAC	TAC	TGG	ATG	ACC	GGC	288
35	Arg	Gly	Glu	Gln	Lys	Ala	His	Leu	Glu	Asp	Tyr	Tyr	Trp	Met	Thr	Gly	
					85					90					95		
	TAC	CCG	CAG	CAG	CTG	AAC	CCC	GAG	GCG	CTG	GGC	TTC	AGC	CCC	GAG	GAC	336
40	Tyr	Pro	Gln	Gln	Leu	Asn	Pro	Glu	Ala	Leu	Gly	Phe	Ser	Pro	Glu	Asp	
				100					105					110			
	GCG	GTC	GAG	GCG	CTC	ATC	AGC	AAC	AGC	CAC	CAG	CTC	CGG	GGC	GGC	TTC	384
45	Ala	Val	Glu	Ala	Leu	Ile	Ser	Asn	Ser	His	Gln	Leu	Arg	Gly	Gly	Phe	
			115					120					125				
	GAT	GGC	TAT	GCG	CGC	GGG	GCG	CAG	CAG	CTA	GCC	GCG	GCG	GCC	GGG	GCA	432
50	Asp	Gly	Tyr	Ala	Arg	Gly	Ala	Gln	Gln	Leu	Ala	Ala	Ala	Ala	Gly	Ala	
		130					135					140					
	GGT	GCC	GGC	GCC	TCC	TTG	GGC	GGC	AGC	GGC	GAG	GAG	ATG	GGC	CCC	GCC	480
55	Gly	Ala	Gly	Ala	Ser	Leu	Gly	Gly	Ser	Gly	Glu	Glu	Met	Gly	Pro	Ala	
	145					150					155					160	

	GCC 528	CCC	GTG	GTG	TCC	GCC	GTG	ATC	GCC	GCG	GCC	GCC	GCG	CAG	AGC	GGC
	Ala	Ala	Val	Val	Ser	Ala	Val	Ile	Ala	Ala	Ala	Ala	Ala	Gln	Ser	Gly
5					165					170					175	
	GCG 576	GGC	CCG	CAC	TAC	CAC	CAC	CAC	CAC	CAC	CAC	GCC	GCC	GGC	CAC	CAC
	Ala	Gly	Pro	His	Tyr	His	His	His	His	His	His	Ala	Ala	Gly	His	His
10				180					185					190		
	CAC 624	CAC	CCG	ACG	GCC	GGC	GCG	CCC	GGC	GCC	GCG	GGC	AGC	GCG	GCC	GCT
	His	His	Pro	Thr	Ala	Gly	Ala	Pro	Gly	Ala	Ala	Gly	Ser	Ala	Ala	Ala
15			195					200					205			
	TCG 672	GCC	GGT	GGC	GCT	GGG	GGC	GCG	GGC	GGC	GGT	GGC	CCG	GCC	AGC	GTT
	Ser	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Gly	Gly	Pro	Ala	Ser	Val
20		210					215					220				
	GGG 720	GGC	GGC	GGC	GGC	GGC	GGC	GGC	GGC	GGA	GGC	GGC	GGG	GGC	GCG	GCG
	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Ala
25		225				230					235					240
	GGC 768	GCC	CTG	CAC	CCG	CAC	CAC	GCC	GCC	GGC	GGC	CTG	CAC	TTC	GAC	GAC
	Gly	Ala	Leu	His	Pro	His	His	Ala	Ala	Gly	Gly	Leu	His	Phe	Asp	Asp
30					245					250					255	
	CGC 816	TTC	TCC	GAC	GAG	CAG	CTG	GTG	ACC	ATG	TCT	GTG	CGC	GAC	TGG	AAC
	Arg	Phe	Ser	Asp	Glu	Gln	Leu	Val	Thr	Met	Ser	Val	Arg	Asp	Trp	Asn
35				260					265					270		
	CGG 864	CAG	CTG	CGC	GGG	GTC	AGC	AAG	GAG	GAG	GTG	ATC	CGG	CTG	AAG	CAG
	Arg	Gln	Leu	Arg	Gly	Val	Ser	Lys	Glu	Glu	Val	Ile	Arg	Leu	Lys	Gln
40			275					280					285			
	AAG 912	AGG	CGG	ACC	CTG	AAA	AAC	CGC	GGC	TAT	GCC	AAG	TCC	TGC	CGC	TTC
	Lys	Arg	Arg	Thr	Leu	Lys	Asn	Arg	Gly	Tyr	Ala	Lys	Ser	Cys	Arg	Phe
45		290					295					300				
	AAG 960	AGG	GTG	CAG	CAG	AGA	CAC	GTC	CTG	GAG	TCG	GAG	AAG	AAC	CAG	CTG
	Lys	Arg	Val	Gln	Gln	Arg	His	Val	Leu	Glu	Ser	Glu	Lys	Asn	Gln	Leu
50		305				310					315					320
	CTG 1008	CAG	CAA	GTC	GAC	CAC	CTC	AAG	CAG	GAG	ATC	TCC	AGG	CTG	GTG	CGC
	Leu	Gln	Gln	Val	Asp	His	Leu	Lys	Gln	Glu	Ile	Ser	Arg	Leu	Val	Arg
55					325					330					335	
	GAG 1056	AGG	GAC	GCG	TAC	AAG	GAG	AAA	TAC	GAG	AAG	TTG	GTG	AGC	AGC	GGC

Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
340 345 350

5 TTC CGA GAA AAC GGC TCG AGC AGC GAC AAC CCG TCC TCT CCC GAG TTT
1104

Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
355 360 365

10 TTC ATA ACT GAG CCC ACT CGC AAG TTG GAG CCA TCA GTG GGA TAC GCC
1152

Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
370 375 380

15 ACA TTT TGG AAG CCC CAG CAT CGT GTA CTT ACC AGT GTG TTC ACA AAA
1200

Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
385 390 395 400

20 TGA
1203

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
1 5 10 15

40 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
20 25 30

Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
35 40 45

45 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
50 55 60

Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
65 70 75 80

50 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
85 90 95

55 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
100 105 110

Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe

[illegible]